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 ccattacgac gaggcggtca ggatgggctc tctgggcctc ttcctgcagt gcgccatcag 1020
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 10 gccctacacc ctggcgctc tgtaccatcg cgagaagcag gtgttcctgc ccaagtaccg 1260
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 caagccgggg gcccttttc ccaacggcca tgtcggggcg ggcggcagcg gcctgtctcc 1380
 tccccccccc gccctgtgcg gcgctagtgc ctggcgacgtg agcgtgcggg tgggtggtggg 1440
 ggagccacc gaggctaggg tcgtgcctgg ccgggggac tgcctggacc tggccatcct 1500
 15 cgactccgcc ttcctgctct ccaggtggc gccagcctg ttcattggga gtatcgtgca 1560
 gctgagccag agcgtgaccg cctacatggt gagcgccgc gcctgggggt tgggtggccat 1620
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 cgaggcag 1688

20 <210> 23
 <211> 435
 <212> DNA
 <213> Artificial Sequence

25 <220>
 <223> Hybrid gene between St. pneum. C-LytA, P2 T helper
 epitope and a small portion of the 5' end of human
 P501S

30 <400> 23
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 aatggcactt ggtactactt tgacagttca ggctatatgc ttgcagaccg ctggagggaag 120
 cacacagacg gcaactggta ctggttcgac aactcaggcg aaatggctac aggctggaag 180
 aaaatcgctg ataagtggta ctatttcaac gaagaagggtg ccatgaagac aggctgggtc 240
 35 aagtacaagg acacttggta ctacttagac gctaaagaag gcgccatgca atacatcaag 300
 gctaactcta agttcattgg tatcactgaa ggcgtcatgg tatcaaatgc ctttatccag 360
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 gaaaagttca tgtac 435

40 <210> 24
 <211> 435
 <212> DNA
 <213> Artificial Sequence

45 <220>
 <223> Hybrid gene between St. pneum. C-LytA, P2 T helper
 epitope and a small portion of the 5' end of human
 P501S - codon-optimised

50 <400> 24
 atggcggccc cctacgtgca tagcgacggg agctacccca aggacaagtt cgagaagatc 60
 aacgggacat ggtactactt cgactcctcc ggctacatgc tcgccgaccg ctggcggaag 120
 cacaccgacg gcaactggta ctggttcgat aactcgggag agatggccac cggctggaag 180
 aagatcgcgg acaagtggta ctatttcaac gaggagggcg ccatgaagac cggctgggtg 240
 55 aagtataagg acacctggta ctacctgac gccaaaggag gcgccatgca gtatatcaag 300
 gccaacagca agttcatcgg catcaccgag ggagtgatgg tcagcaacgc ctttatccag 360
 agcgccgacg gcaccgatg gtactacttg aagccggacg gcaccctcgc ggatcgggcc 420
 gagaagttca tgtac 435

60 <210> 25
 <211> 435

<212> DNA

<213> Artificial Sequence

<220>

- 5 <223> Hybrid gene between St. pneum. C-LytA, P2 T helper epitope and a small portion of the 5' end of human P501S - codon-optimised

<400> 25

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10 atggccgccc cctacgtgca cagcgacggg tcctacccaa aggacaagtt cgagaagatc 60
   aacggcacgt ggtactatct cgacagcagc ggctacatgc tcgccgatcg ctggcgcaag 120
   cacaccgacg ggaactggta ctggttcgac aactctggcg agatggctac ggggtggaag 180
   aagatcgccc acaagtggta ctacttcaac gaggagggcg ccatgaagac cgggtgggtg 240
   aagtacaagg acacctggta ctacctggac gctaaggagg gcgccatgca gtacatcaag 300
15 gccaaactga agttcatcgg gatcaccgag ggcgtgatgg tcagtaacgc ttcatccag 360
   agcgcggacg gcacaggctg gtattacctg aagcccgatg gcaccctggc ggacagacct 420
   gagaaattca tgtac                                     435

```

<210> 26

20 <211> 464

<212> DNA

<213> Artificial Sequence

<220>

- 25 <223> Hybrid gene between St. pneum. C-LytA, P2 T helper epitope and a small portion of the 5' end of human P501S - codon-optimised

<400> 26

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30 gacggctagc gccaccatgg ccgcccgccta cgtgcatagc gacgggagct accccaagga 60
   caagttcagc aagatcaacg ggacatggta ctacttcgac tcctccggct acatgctcgc 120
   cgaccgctgg cggaagcaca ccgacggcaa ctggtactgg ttcgataact cgggagagat 180
   ggccaccggc tggaagaaga tcgcggaaca gtggtactat ttcaacgagg agggcgccat 240
   gaagaccggc tgggtgaagt ataaggacac ctggtactac ctcgacgcca aggagggcgc 300
35 catgcagtat atcaaggcca acagcaagtt catcggcac accgagggag tgatggtcag 360
   caacgccttt atccagagcg ccgacggcac cggatggtac tacttgaagc cggacggcac 420
   cctcgccgat cggcccgaga agttcatgta ctgactcgag gcag                                     464

```

<210> 27

40 <211> 652

<212> PRT

<213> Artificial Sequence

<220>

- 45 <223> Hybrid protein between St. pneum. C-LytA, P2 T helper epitope and amino acids 51-553 of human P501S

<400> 27

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50 Met Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp Lys
   1           5           10           15
   Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr
           20           25           30
   Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
55           35           40           45
   Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
           50           55           60
   Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
           65           70           75           80
60 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
           85           90           95

```

	Gln	Tyr	Ile	Lys	Ala	Asn	Ser	Lys	Phe	Ile	Gly	Ile	Thr	Glu	Gly	Val
				100					105					110		
	Met	Val	Ser	Asn	Ala	Phe	Ile	Gln	Ser	Ala	Asp	Gly	Thr	Gly	Trp	Tyr
			115					120					125			
5	Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys	Phe	Met
		130					135					140				
	Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys	Val	Pro
	145					150					155				160	
	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly	Arg	Tyr	Gly	Arg	Arg
				165						170					175	
10	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser	Leu	Phe
			180						185					190		
	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro	Asp	Pro
			195					200					205			
15	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly	Val	Gly	Leu	Leu	Asp
	210						215					220				
	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser	Asp
	225					230					235					240
	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val	Tyr	Ala
				245						250					255	
20	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala	Ile
			260						265					270		
	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Glu
			275					280					285			
25	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val	Ala	Ala
		290					295					300				
	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala
	305					310					315				320	
	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro	Cys	Arg
				325						330					335	
30	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg	Leu	His
			340						345					350		
	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	Val	Ala
			355					360						365		
35	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe	Tyr	Thr
		370					375					380				
	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala	Glu	Pro
	385					390					395					400
	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser
				405						410					415	
40	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val
				420					425					430		
	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr	Leu	Ala
			435					440					445			
45	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His
		450					455					460				
	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu	Thr	Gly	Phe	Thr	Phe
	465					470					475					480
	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala	Ser	Leu	Tyr	His	Arg
				485						490					495	
50	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly	Asp	Thr	Gly	Gly	Ala
				500					505					510		
	Ser	Ser	Glu	Asp	Ser	Leu	Met	Thr	Ser	Phe	Leu	Pro	Gly	Pro	Lys	Pro
			515					520					525			
55	Gly	Ala	Pro	Phe	Pro	Asn	Gly	His	Val	Gly	Ala	Gly	Gly	Ser	Gly	Leu
		530					535					540				
	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly	Ala	Ser	Ala	Cys	Asp	Val	Ser
	545					550					555					560
	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly
					565					570					575	
60	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile	Leu	Asp	Ser	Ala	Phe	Leu	Leu

580 585 590
 Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser
 595 600 605
 Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val
 610 615 620
 5 Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala
 625 630 635 640
 Lys Tyr Ser Ala Gly Gly His His His His His
 645 650
 10
 <210> 28
 <211> 1959
 <212> DNA
 15 <213> Artificial Sequence
 <220>
 <223> DNA encoding the Hybrid protein between St. pneum.
 C-LytA, P2 T helper epitope and amino acids 51-553
 20 of human P501S
 <400> 28
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 aatggcactt ggtactactt tgacagttca ggctatatgc ttgcagaccg ctggaggaag 120
 25 cacacagacg gcaactggta ctggttcgac aactcaggcg aaatggctac aggctggaag 180
 aaaatcgctg ataagtggta ctatttcaac gaagaagggtg ccatgaagac aggtcgggtc 240
 aagtacaagg acacttggta ctacttagac gctaaagaag gcgccatgca ataatcaag 300
 gctaaactcta agttcattgg tatcactgaa ggcgtcatgg tatcaaatgc ctttatccag 360
 tcagcggacg gaacaggctg gtactacctc aaaccagacg gaacactggc agacaggcca 420
 30 gaaaagtcca tgtacatggg gctgggcatt ggtccagtgc tgggcctggg ctgtgtcccg 480
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 gcagggctgc tgtgcccgga tcccaggccc ctggagctgg cactgctcat cctgggctgt 660
 gggctgctgg acttctgtgg ccagggtgag ttcactccac tggaggccct gctctctgag 720
 35 ctcttcgggg acccggaaca ctgtcgccag gcctactctg tctatgcctt catgatcagt 780
 cttgggggct gcctgggcta cctcctgcct gccattgact gggacaccag tggcctggcc 840
 ccctacctgg gacccagga ggagtgcttc tttggcctgc tcaccctcat cttcctcacc 900
 tgcgtagcag ccacactgct ggtggctgag gaggcagcgc tgggccccac cgagccagca 960
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 40 ttccggaacc tgggcgccc gcttccccgg ctgcaccagc tgtgctgccc catgccccgc 1080
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 ggcaccgagg cccggagaca ctatgatgaa ggcgttcgga tgggcagcct ggggctgttc 1260
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 45 ggcactcgag cagtctatct ggccagtgtg gcagctttcc ctgtggctgc cgggtgccaca 1380
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 50 ggcagtggcc tgctcccacc tccaccgcg ctctgcgggg cctctgcctg tgatgtctcc 1680
 gtacgtgtgg ttgtgggtga gcccaccgag gccagggtgg ttccgggccc gggcatctgc 1740
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 atgggtccca tgtccagct cagccagtct gtcactgcct atatggtgtc tgccgcaggc 1860
 ctgggtctgg tggccattta ctttgttaca caggtagtat ttgacaagag cgacttggcc 1920
 55 aaatactcag cgggtggaca ccatcaccat caccattaa 1959
 <210> 29
 <211> 507
 <212> PRT
 60 <213> Artificial Sequence

<220>

<223> Human P501S (amino acids 55-553) fused to 6 histidine residues

5 <400> 29
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 Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
 20 25 30
 10 Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe Leu
 35 40 45
 Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro Arg
 50 55 60
 Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp Phe
 65 70 75 80
 15 Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp Leu
 85 90 95
 Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala Phe
 100 105 110
 20 Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile Asp
 115 120 125
 Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu Cys
 130 135 140
 Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala Thr
 145 150 155 160
 25 Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala Glu
 165 170 175
 Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg Ala
 180 185 190
 30 Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His Gln
 195 200 205
 Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala Glu
 210 215 220
 Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr Asp
 225 230 235 240
 35 Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro Gly
 245 250 255
 Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser Leu
 260 265 270
 40 Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val Met
 275 280 285
 Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala Ser
 290 295 300
 Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His Ser
 305 310 315 320
 45 Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe Ser
 325 330 335
 Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg Glu
 340 345 350
 50 Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala Ser
 355 360 365
 Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro Gly
 370 375 380
 Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu Leu
 385 390 395 400
 55 Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser Val
 405 410 415
 Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly Arg
 420 425 430
 60 Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu Ser
 435 440 445

Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser Gln
 450 455 460
 Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val Ala
 465 470 475 480
 5 Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala Lys
 485 490 495
 Tyr Ser Ala Gly His His His His His His
 500 505

10 <210> 30
 <211> 1524
 <212> DNA
 <213> Artificial Sequence

15 <220>
 <223> DNA encoding Human P501S (amino acids 55-553)
 fused to 6 histidine residues

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 ggcattcctgc tgagcctctt tctcatccca agggccggct ggctagcagg gctgctgtgc 180
 ccgcatccca ggcccctgga gctggcactg ctcatcctgg gcgtggggct gctggacttc 240
 25 tgtggccagg tgtgtctcac tccactggag gccctgtctt ctgacctctt ccgggaccgc 300
 gaccactgtc gccaggccta ctctgtctat gccttcata tcagtcttgg gggctgcctg 360
 ggctacctcc tgcctgcat tgactgggac accagtgcct tggcccccta cctgggcacc 420
 caggaggagt gcctctttgg cctgctcacc ctcatcttcc tcacctgctt agcagccaca 480
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 30 ccttccttgt cgccccactg ctgtccatgc cgggcccgc tggccttccg gaacctgggc 600
 gccctgcttc ccgggctgca ccagctgtgc tgccgcatgc cccgcacct gcgcccgtc 660
 ttcgtggctg agctgtgcag ctggatggca ctcatgacct tcacgtgtt ttacacggat 720
 ttcgtgggctg aggggctgta ccaggcgctg ccagagctg agccgggcac cgaggcccgc 780
 agacactatg atgaaggcgt tcggatgggc agcctggggc tgttcctgca gtgcgccatc 840
 35 tccctggctc tctctctggt catggaccgg ctggtgcagc gattcggcac tcgagcagtc 900
 tatttggcca gtgtggcagc tttccctgtg gctgccggtg ccacatgcct gtcccacagt 960
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 40 cctaagcctg gagctccctt ccctaagga cactggtgtg ctggaggcag tggcctgtc 1200
 ccacctccac ccgctctctg cggggcctct gcctgtgatg tctccgtacg tgtggtggtg 1260
 ggtgagccca ccgaggccag ggtggttccg gccgggggca tctgcctgga cctcgccatc 1320
 ctggatagtg ccttctgtct gtcccagggt gcccacatcc tgtttatggg ctccattgtc 1380
 cagctcagcc agtctgtcac tgcctatatg gtgtctgccg caggcctggg tctgggtcgc 1440
 45 atttactttg ctacacaggt agtatattgac aagagcgact tggccaaata ctcagcgggt 1500
 ggacaccatc accatcacca ttaa 1524

<210> 31
 <211> 685
 50 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Human P501S (amino acids 1-34 fused to 55-553)
 55 fused to 6 histidine residues

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 60 Lys Ala Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val
 20 25 30

Cys Leu Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro Lys Asp
 35 40 45
 Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly
 50 55 60
 5 Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr
 65 70 75 80
 Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala
 85 90 95
 Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp
 100 105 110
 10 Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala
 115 120 125
 Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly
 130 135 140
 15 Val Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp
 145 150 155 160
 Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe
 165 170 175
 Met Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val
 180 185 190
 20 Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg
 195 200 205
 Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu
 210 215 220
 25 Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp
 225 230 235 240
 Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu
 245 250 255
 Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser
 260 265 270
 30 Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr
 275 280 285
 Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala
 290 295 300
 35 Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu
 305 310 315 320
 Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala
 325 330 335
 Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro
 340 345 350
 40 Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys
 355 360 365
 Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu
 370 375 380
 45 His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val
 385 390 395 400
 Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr
 405 410 415
 Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu
 420 425 430
 50 Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly
 435 440 445
 Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu
 450 455 460
 55 Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu
 465 470 475 480
 Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser
 485 490 495
 His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr
 500 505 510
 60 Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His

515 520 525
 Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly
 530 535 540
 5 Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys
 545 550 555 560
 5 Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly
 565 570 575
 Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val
 580 585 590
 10 Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro
 595 600 605
 Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu
 610 615 620
 Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu
 625 630 635 640
 15 Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu
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 Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu
 660 665 670
 20 Ala Lys Tyr Ser Ala Gly Gly His His His His His His
 675 680 685

 <210> 32
 25 <211> 2058
 <212> DNA
 <213> Artificial Sequence

 <220>
 30 <223> DNA encoding Human P501S (amino acids 1-34 fused
 to 55-553) fused to 6 histidine residues

 <400> 32
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 35 ttggttggtta acttggttgac cttcgggctg gaagtctggt tggcggccgc ttacgtacat 120
 tccgacggct cttatccaaa agacaagttt gagaaaatca atggcacttg gtactacttt 180
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 45 ctgctgagcc tctttctcat cccaagggcc ggctggctag cagggtgctg gtgcccggat 720
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catcaccatc accattaa                                     2058

<210> 33
10 <211> 671
    <212> PRT
    <213> Artificial Sequence

<220>
15 <223> St. pneum. C-LytA portion fused to P2 T helper
    epitope fused to Human P501S (amino acids 55-553)
    fused to 6 histidine residues downstream of yeast
    alphaprepro signal sequence

20 <400> 33
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      1           5           10           15
    Ser Ser Ala Leu Ala Ala Ala Tyr Val His Ser Asp Gly Ser Tyr Pro
      20           25           30
25 Lys Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser
      35           40           45
    Ser Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn
      50           55           60
    Trp Tyr Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys
      65           70           75           80
30 Ile Ala Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr
      85           90           95
    Gly Trp Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu
      100          105          110
35 Gly Ala Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr
      115          120          125
    Glu Gly Val Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr
      130          135          140
    Gly Trp Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu
      145          150          155          160
40 Lys Phe Met Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val
      165          170          175
    Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr
      180          185          190
45 Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu
      195          200          205
    Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys
      210          215          220
    Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly Val Gly
      225          230          235          240
50 Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu
      245          250          255
    Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser
      260          265          270
55 Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu
      275          280          285
    Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr
      290          295          300
    Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys
      305          310          315          320
60 Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr

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5  Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro
      355      360      365
Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu
      370      375      380
Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu
385      390      395      400
10 Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg
      405      410      415
Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg
      420      425      430
15 Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe
      435      440      445
Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val
450      455      460
Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys
465      470      475      480
20 Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly
      485      490      495
Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu
500      505      510
Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr
25      515      520      525
Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly
530      535      540
Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly
545      550      555      560
30 Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys
565      570      575
Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val
580      585      590
35 Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala
595      600      605
Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val
610      615      620
Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu
625      630      635      640
40 Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser
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Asp Leu Ala Lys Tyr Ser Ala Gly Gly His His His His His His
660      665      670

45 <210> 34
    <211> 2477
    <212> DNA
    <213> Artificial Sequence

50 <220>
    <223> DNA encoding St. pneum. C-LytA portion fused to P2
        T helper epitope fused to Human P501S (amino acids
        55-553) fused to 6 histidine residues downstream
55 of yeast alphaprepro signal sequence

    <400> 34
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60 aactgggtact ggttcgacaa ctcaggcgaa atggctacag gctggaagaa aatcgctgat 180
    aagtgggtact atttcaacga agaaggtgcc atgaagacag gctgggtcaa gtacaaggac 240

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acaggctggt actacctcaa accagacgga acactggcag acaggccaga aatggcggcc 420
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5  tacgtacatt ccgacggctc ttatccaaaa gacaagtttg agaaaatcaa tggcacttgg 540
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atcaccatca ccattaa 2477

40  <210> 35
    <211> 595
    <212> PRT
    <213> Artificial Sequence

45  <220>
    <223> Human P501S (amino acids 55-553) fused to 6
        histidine residues downstream of yeast alphaprepro
        signal sequence

50  <400> 35
    Met Ser Phe Leu Asn Phe Thr Ala Val Leu Phe Ala Ala Ser Ser Ala
      1           5           10          15
    Leu Ala Ala Pro Val Asn Thr Thr Thr Glu Asp Glu Thr Ala Gln Ile
      20           25           30
55  Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe Asp
      35           40           45
    Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu Phe
      50           55           60
    Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val Ser
      65           70           75           80
60  Leu Glu Lys Arg Glu Ala Glu Ala Met Val Leu Gly Ile Gly Pro Val

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5	Arg	Gly	Arg	Tyr	Gly	Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu
			115				120						125			
	Gly	Ile	Leu	Leu	Ser	Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala
		130					135					140				
	Gly	Leu	Leu	Cys	Pro	Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile
		145				150					155					160
10	Leu	Gly	Val	Gly	Leu	Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro
				165						170						175
	Leu	Glu	Ala	Leu	Leu	Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg
				180					185					190		
	Gln	Ala	Tyr	Ser	Val	Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu
			195				200						205			
15	Gly	Tyr	Leu	Leu	Pro	Ala	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro
		210					215						220			
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		225			230						235					240
20	Phe	Leu	Thr	Cys	Val	Ala	Ala	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala
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25	Pro	His	Cys	Cys	Pro	Cys	Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly
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30	Thr	Phe	Thr	Leu	Phe	Tyr	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln
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	Gly	Val	Pro	Arg	Ala	Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp
				340				345						350		
35	Glu	Gly	Val	Arg	Met	Gly	Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile
		355					360						365			
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		370					375					380				
	Thr	Arg	Ala	Val	Tyr	Leu	Ala	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala
		385				390					395					400
40	Gly	Ala	Thr	Cys	Leu	Ser	His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala
				405						410						415
	Ala	Leu	Thr	Gly	Phe	Thr	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr
			420					425						430		
45	Leu	Ala	Ser	Leu	Tyr	His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr
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		450				455					460					
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		465				470					475					480
50	Gly	Ala	Gly	Gly	Ser	Gly	Leu	Leu	Pro	Pro	Pro	Pro	Ala	Leu	Cys	Gly
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	Ala	Ser	Ala	Cys	Asp	Val	Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr
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55	Glu	Ala	Arg	Val	Val	Pro	Gly	Arg	Gly	Ile	Cys	Leu	Asp	Leu	Ala	Ile
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	Leu	Asp	Ser	Ala	Phe	Leu	Leu	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met
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	Gly	Ser	Ile	Val	Gln	Leu	Ser	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser
		545				550					555					560
60	Ala	Ala	Gly	Leu	Gly	Leu	Val	Ala	Ile	Tyr	Phe	Ala	Thr	Gln	Val	Val
				565					570						575	

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10

15

20

50

55

60

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<210> 38
<211> 2045
35 <212> DNA
    <213> Artificial Sequence

<220>
<223> DNA encoding codon-optimised Human P501S (amino acids 1-553)
40 fused to St.pneum. C-LytA P2 helper epitope C-Lyta

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60 tgctggtggc cgaggaggcg gccctggggc ccaccgagcc cgcagaggcg ctgagcgctc 1080
ccagcctgag ccccatctgc tgcccgtgca gggctagggt cgccttcagg aatctggggc 1140

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agctgagcca gagcgtgacc gcctacatgg tgagcgccgc cggcctgggg ttgggtggcca 1980
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gatcc 2045

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<210> 39

<211> 2105

20 <212> DNA

<213> Artificial Sequence

<220>

25 <223> DNA encoding St.pneum. C-LytA P2 helper epitope
C-Lyta fused to Human P501S (amino acids 51-553)
fused to Human P501S (amino acids 1-50) -
Codon-optimised

<400> 39

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30 gcgccgcgcg caccatggcc gccgcctacg tgcatagcga cgggagctac cccaaggaca 60
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accgctggcg gaagcacacc gacggcaact ggtactgggt cgataactcg ggagagatgg 180
ccaccggctg gaagaagatc gcggacaagt ggtactatct caacgaggag ggcgccatga 240
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35 tgcagtatat caaggccaac agcaagtcca tcggcatcac cgagggaagt atggtcagca 360
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55 gcgagaagca ggtgttcctg cccaagtacc gcggggacac agggggagct tcctctgagg 1560
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60 cgcccagcct gttcatgggc agtatcgtgc agctgagcca gagcgtgacc gcctacatgg 1860
tgagcgccgc cggcctgggg ttgggtggcca tctactttgc caccaggtc gtgttcgaca 1920

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agagcgatct cgccaagtat agcgccatgg tgcagcggct gtgggtgtcc cggctgctgc 1980
gccatagaaa ggcccagttg ctgctggtga acctgctgac tttcggactg gaggtgtgcc 2040
tggctgccgg gatcacgtac gtgccccccc tgetgctgga ggtgggcgtg gaggagttag 2100
gatcc 2105

5 <210> 40
  <211> 2105
  <212> DNA
  <213> Artificial Sequence

10 <220>
  <223> DNA encoding Human P501S (amino acids 1-50) fused
      to St.pneum. C-LyTA P2 helper epitope C-Lyta fused
      to Human P501S (amino acids 51-553) -
15 Codon-optimised

  <400> 40
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cccagttgct gctggtgaac ctgctgactt tcggactgga ggtgtgcctg gctgccggga 120
20 tcacgtacgt gccccccctg ctgctggagg tgggcgtgga ggagatggcc gccgcctacg 180
tgcatacgca cgggagctac cccaaggaca agttcgagaa gatcaacggg acatgggtact 240
acttcgactc ctccggctac atgctcgccg accgctggcg gaagcacacc gacggcaact 300
ggtactgggt cgataactcg ggagagatgg ccaccggctg gaagaagatc gcggacaagt 360
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25 ggtactacct cgacgccaaag gagggcgcca tgcagtatat caaggccaac agcaagttca 480
tcggcatcac cgagggagtg atggtcagca acgcctttat ccagagcgcc gacggcaccg 540
gatgggtacta cttgaagccg gacggcaccc tcgcggtatcg gcccgagaag ttcattgtaca 600
tgggtgctggg catcgcccc gtctctgggc tcgtgtgtgt gcccctcctc gggagtgcgt 660
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50 tcgactccgc cttcctgctc tcccagggtg cgcacagcct gttcatgggc agtatcgtgc 1980
agctgagcca gacgtgacc gcctacatgg tgagcgccgc cggcctgggg ttggtggcca 2040
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gatcc 2105

55 <210> 41
  <211> 652
  <212> PRT
  <213> Artificial Sequence

60 <220>
  <223> St.pneum. C-LyTA P2 helper epitope C-Lyta fused to

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Human P501S

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<400> 41
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    Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr Phe Asp Ser Ser Gly Tyr
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10  Met Leu Ala Asp Arg Trp Arg Lys His Thr Asp Gly Asn Trp Tyr Trp
    35      40      45
    Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
    50      55      60
    Lys Trp Tyr Tyr Phe Asn Glu Gly Ala Met Lys Thr Gly Trp Val
    65      70      75      80
    Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
    85      90      95
15  Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val
    100      105      110
    Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
    115      120      125
20  Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met
    130      135      140
    Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro
    145      150      155      160
    Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
    165      170      175
25  Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe
    180      185      190
    Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro
    195      200      205
30  Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly Val Gly Leu Leu Asp
    210      215      220
    Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu Leu Ser Asp
    225      230      235      240
    Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala
    245      250      255
35  Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu Pro Ala Ile
    260      265      270
    Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu
    275      280      285
40  Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala
    290      295      300
    Thr Leu Leu Val Ala Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala
    305      310      315      320
    Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg
    325      330      335
45  Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu Leu Pro Arg Leu His
    340      345      350
    Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala
    355      360      365
50  Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr
    370      375      380
    Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro
    385      390      395      400
    Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser
    405      410      415
55  Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val
    420      425      430
    Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
    435      440      445
60  Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His
    450      455      460

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Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe
 465 470 475 480
 Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg
 485 490 495
 5 Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala
 500 505 510
 Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro
 515 520 525
 10 Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu
 530 535 540
 Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser Ala Cys Asp Val Ser
 545 550 555 560
 Val Arg Val Val Val Gly Glu Pro Thr Glu Ala Arg Val Val Pro Gly
 565 570 575
 15 Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala Phe Leu Leu
 580 585 590
 Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val Gln Leu Ser
 595 600 605
 20 Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val
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 625 630 635 640
 Lys Tyr Ser Ala Gly Gly His His His His His His
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25

<210> 42

<211> 1959

<212> DNA

30 <213> Artificial Sequence

<220>

 <223> DNA encoding St.pneum. C-LytA P2 helper epitope
 C-Lyta fused to Human P501S (plus his tag)

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<400> 42

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 cacacagacg gcaactggta ctggttcgac aaactcaggcg aaatggctac aggcctggaag 180
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 tgcgtagcag ccacactgct ggtggctgag gaggcagcgc tgggccccac cgagccagca 960
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aaatactcag cgggtgggaca ccatcaccat caccattaa 1959

10 <210> 43
    <211> 553
    <212> PRT
    <213> Homo sapiens

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      20           25           30
20 Ala Ala Gly Ile Thr Tyr Val Pro Leu Leu Leu Glu Val Gly Val
      35           40           45
    Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
      50           55           60
    Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
25 65           70           75           80
    Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
      85           90           95
    Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
      100          105          110
30 Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
      115          120          125
    Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
      130          135          140
    Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
35 145          150          155          160
    Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
      165          170          175
    Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
      180          185          190
40 Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
      195          200          205
    Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
      210          215          220
    Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
45 225          230          235          240
    Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
      245          250          255
    Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
      260          265          270
50 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
      275          280          285
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      290          295          300
    Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
55 305          310          315          320
    Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
      325          330          335
    Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
      340          345          350
60 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
      355          360          365

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 385 390 395 400
 5 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 10 Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 15 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
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 545 550
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 30 <213> Artificial Sequence
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 Human P501S
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 20 25 30
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 35 40 45
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
 50 55 60
 45 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
 65 70 75 80
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
 85 90 95
 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val
 100 105 110
 50 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
 115 120 125
 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met
 130 135 140
 55 Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro
 145 150 155 160
 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
 165 170 175
 Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe
 180 185 190
 60 Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro

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	210						215				220					
	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu	Ser	Asp
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					245					250					255	
	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro	Ala	Ile
				260					265					270		
10	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln	Glu	Glu
			275					280					285			
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		290					295					300				
	Thr	Leu	Leu	Val	Ala	Glu	Glu	Ala	Ala	Leu	Gly	Pro	Thr	Glu	Pro	Ala
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	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met	Gly	Ser
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	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser	Leu	Val
				420					425					430		
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			435					440					445			
	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala	Thr	Cys	Leu	Ser	His
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	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala	Arg	Val	Val	Pro	Gly
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50	Ser	Gln	Val	Ala	Pro	Ser	Leu	Phe	Met	Gly	Ser	Ile	Val	Gln	Leu	Ser
				595					600					605		
	Gln	Ser	Val	Thr	Ala	Tyr	Met	Val	Ser	Ala	Ala	Gly	Leu	Gly	Leu	Val
		610					615						620			
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60 <210> 45
 <211> 644

<212> PRT

<213> Artificial Sequence

<220>

- 5 <223> Codon-optimised hybrid protein between St.pneum. C-LyTA P2
 helper epitope C-Lyta fused to Human P501S
 amino acids 51-553)

<400> 45

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    50      55      60
    Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
    65      70      75      80
20 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
    85      90      95
    Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val
    100      105      110
    Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
    115      120      125
25 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Lys Phe Met
    130      135      140
    Tyr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val Cys Val Pro
    145      150      155      160
30 Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr Gly Arg Arg
    165      170      175
    Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu Ser Leu Phe
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    Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys Pro Asp Pro
    195      200      205
35 Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly Leu Leu Asp
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40 Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser Val Tyr Ala
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    260      265      270
    Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr Gln Glu Glu
    275      280      285
45 Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu Thr Cys Val Ala Ala
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    Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly Pro Thr Glu Pro Ala
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50 Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His Cys Cys Pro Cys Arg
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    Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala
    355      360      365
55 Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr
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    385      390      395      400
60 Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser
    405      410      415

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 595 600 605
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<210> 46
 <211> 694
 35 <212> PRT
 <213> Artificial Sequence

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 <223> St. pneumoniae C-LytA P2 helper epitope C-LytA fused to
 40 Human P501S (amino acids 1-553)- codon optimised

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 35 40 45
 Phe Asp Asn Ser Gly Glu Met Ala Thr Gly Trp Lys Lys Ile Ala Asp
 50 55 60
 Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala Met Lys Thr Gly Trp Val
 65 70 75 80
 Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp Ala Lys Glu Gly Ala Met
 85 90 95
 55 Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu Gly Val
 100 105 110
 Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp Gly Thr Gly Trp Tyr
 115 120 125
 Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Arg Pro Glu Met Val Gln
 130 135 140
 60 Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala Gln Leu Leu

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					165					170			175
	Ile	Thr	Tyr	Val	Pro	Pro	Leu	Leu	Leu	Glu	Val	Gly	Val
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	Phe	Met	Thr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly
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	Val	Pro	Leu	Leu	Gly	Ser	Ala	Ser	Asp	His	Trp	Arg	Gly
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10	Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile
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	Asp	Pro	Arg	Pro	Leu	Glu	Leu	Ala	Leu	Leu	Ile	Leu	Gly
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	Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu
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	Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala
		290				295					300		
20	Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr
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	Leu	His	Gln	Leu	Cys	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg
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	Tyr	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val
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	Glu	Pro	Gly	Thr	Glu	Ala	Arg	His	Tyr	Asp	Glu	Gly	Val
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	Leu	Val	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg
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45	Leu	Ala	Ser	Val	Ala	Ala	Phe	Pro	Val	Ala	Ala	Gly	Ala
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	Ser	His	Ser	Val	Ala	Val	Val	Thr	Ala	Ser	Ala	Ala	Leu
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	Thr	Phe	Ser	Ala	Leu	Gln	Ile	Leu	Pro	Tyr	Thr	Leu	Ala
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50	His	Arg	Glu	Lys	Gln	Val	Phe	Leu	Pro	Lys	Tyr	Arg	Gly
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	Val	Ser	Val	Arg	Val	Val	Val	Gly	Glu	Pro	Thr	Glu	Ala
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32

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 5 Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg Arg Leu Phe Val Ala
 355 360 365
 Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe Thr Leu Phe Tyr Thr
 370 375 380
 10 Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val Pro Arg Ala Glu Pro
 385 390 395 400
 Gly Thr Glu Ala Arg His Tyr Asp Glu Gly Val Arg Met Gly Ser
 405 410 415
 Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu Val Phe Ser Leu Val
 420 425 430
 15 Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg Ala Val Tyr Leu Ala
 435 440 445
 Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala Thr Cys Leu Ser His
 450 455 460
 20 Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu Thr Gly Phe Thr Phe
 465 470 475 480
 Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr His Arg
 485 490 495
 Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr Gly Gly Ala
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 25 Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly Pro Lys Pro
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 Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala Gly Gly Ser Gly Leu
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 565 570 575
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 Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly Leu Val
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 40 Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser Asp Leu Ala
 625 630 635 640
 Lys Tyr Ser Ala Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg
 645 650 655
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<210> 48
 <211> 694
 <212> PRT
 <213> Artificial Sequence

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<220>
 <223> Human P501S (amino acids 1-50) fused to St.pneum.
 C-LytA P2 helper epitope C-Lyta fused to Human
 P501S (amino acids 51-553) - codon optimised

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				20					25					30		
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	Gly	Tyr	Met	Leu	Ala	Asp	Arg	Trp	Arg	Lys	His	Thr	Asp	Gly	Asn	Trp
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	Tyr	Trp	Phe	Asp	Asn	Ser	Gly	Glu	Met	Ala	Thr	Gly	Trp	Lys	Lys	Ile
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	Trp	Tyr	Tyr	Leu	Lys	Pro	Asp	Gly	Thr	Leu	Ala	Asp	Arg	Pro	Glu	Lys
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25	Phe	Met	Tyr	Met	Val	Leu	Gly	Ile	Gly	Pro	Val	Leu	Gly	Leu	Val	Cys
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		210					215					220				
30	Arg	Arg	Arg	Pro	Phe	Ile	Trp	Ala	Leu	Ser	Leu	Gly	Ile	Leu	Leu	Ser
	225					230					235					240
	Leu	Phe	Leu	Ile	Pro	Arg	Ala	Gly	Trp	Leu	Ala	Gly	Leu	Leu	Cys	Pro
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35	Leu	Asp	Phe	Cys	Gly	Gln	Val	Cys	Phe	Thr	Pro	Leu	Glu	Ala	Leu	Leu
			275						280					285		
	Ser	Asp	Leu	Phe	Arg	Asp	Pro	Asp	His	Cys	Arg	Gln	Ala	Tyr	Ser	Val
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	Tyr	Ala	Phe	Met	Ile	Ser	Leu	Gly	Gly	Cys	Leu	Gly	Tyr	Leu	Leu	Pro
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	Ala	Ile	Asp	Trp	Asp	Thr	Ser	Ala	Leu	Ala	Pro	Tyr	Leu	Gly	Thr	Gln
					325					330					335	
	Glu	Glu	Cys	Leu	Phe	Gly	Leu	Leu	Thr	Leu	Ile	Phe	Leu	Thr	Cys	Val
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	Pro	Ala	Glu	Gly	Leu	Ser	Ala	Pro	Ser	Leu	Ser	Pro	His	Cys	Cys	Pro
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	Cys	Arg	Ala	Arg	Leu	Ala	Phe	Arg	Asn	Leu	Gly	Ala	Leu	Leu	Pro	Arg
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	Leu	His	Gln	Leu	Cys	Arg	Met	Pro	Arg	Thr	Leu	Arg	Arg	Leu	Phe	
					405				410					415		
	Val	Ala	Glu	Leu	Cys	Ser	Trp	Met	Ala	Leu	Met	Thr	Phe	Thr	Leu	Phe
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55	Tyr	Thr	Asp	Phe	Val	Gly	Glu	Gly	Leu	Tyr	Gln	Gly	Val	Pro	Arg	Ala
			435					440					445			
	Glu	Pro	Gly	Thr	Glu	Ala	Arg	Arg	His	Tyr	Asp	Glu	Gly	Val	Arg	Met
		450					455					460				
	Gly	Ser	Leu	Gly	Leu	Phe	Leu	Gln	Cys	Ala	Ile	Ser	Leu	Val	Phe	Ser
60	465					470					475					480
	Leu	Val	Met	Asp	Arg	Leu	Val	Gln	Arg	Phe	Gly	Thr	Arg	Ala	Val	Tyr

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 5 Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala Ser Leu Tyr
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 Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu Gly
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 <212> DNA
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 P2 helper epitope C-LytA

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10 attggtatca ctgaaggcgt catggtatca aatgccttta tccagtcagc ggacggaaca 1920
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15 <212> PRT

<213> Artificial Sequence

<220>

20 <223> Human MUC-1 fused to St.pneum. C-Lyta P2 helper
epitope C-Lyta

<400> 50

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Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
1      5      10      15
25 Val Leu Thr Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
      20      25      30
Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
      35      40      45
30 Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
      50      55      60
Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
65      70      75      80
Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
      85      90      95
35 Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
      100      105      110
Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
      115      120      125
40 Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
      130      135      140
Arg Pro Pro Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
145      150      155      160
Ala Pro Asp Thr Arg Pro Pro Pro Gly Ser Thr Ala Pro Ala Ala His
      165      170      175
45 Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
      180      185      190
Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu
      195      200      205
50 Ala Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser
      210      215      220
Ala Ser Gly Ser Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg
225      230      235      240
Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser
      245      250      255
55 His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
      260      265      270
Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
      275      280      285
60 Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
      290      295      300
Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp

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37

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atcaaggcta actctaagtt cattgggtatc actgaaggcg tcatgggtatc aaatgccttt 420
atccagtcag cggacggaac aggctgggtac tacctcaaac cagacggaac actggcagac 480
aggccagaaa tgacaccggg caccagtcct cctttcttcc tgctgctgct cctcacagtg 540
cttacagttg ttacaggttc tggatcatgca agctctaccc caggtggaga aaaggagact 600
5 tcggtacccc agagaagttc agtgcccagc tctactgaga agaatgctgt gagtatgacc 660
agcagcgtac tctccagcca cagccccggt tcaggctcct ccaccactca gggacaggat 720
gtcactctgg ccccgccac ggaaccagct tcaggttcag ctgccacctg gggacaggat 780
gtcacctcgg tcccagtcac caggccagcc ctgggctcca ccaccgcc agcccacgat 840
gtcacctcag ccccgacaa caagccagcc cggggtcca ccgcccccc agcccacggt 900
10 gtcacctcgg ccccgacac caggccgccc ccgggctcca ccgcccccc agcccacggt 960
gtcacctcgg ccccgacac caggccgccc ccgggctcca ccgcccccc agcccacggt 1020
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15 tctgccaggg ctaccacaac ccagccagc aagagcactc cattctcaat tcccagccac 1260
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tatgtgcccc ctagcagtag cgatcgtagc ccctatgaga aggtttctgc aggtaatggt 1980
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30 <210> 52
    <211> 678
    <212> PRT
    <213> Artificial Sequence

35 <220>
    <223> St.pneum. C-LytA P2 helper epitope C-Lyta fused
        to Human MUC-1

40 <400> 52
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly
  1          5          10          15
Val His Ser Gln Val Gln Met Ala Ala Tyr Val His Ser Asp Gly
  20          25          30
Ser Tyr Pro Lys Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr
45          35          40          45
Phe Asp Ser Ser Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr
  50          55          60
Asp Gly Asn Trp Tyr Trp Phe Asp Asn Ser Gly Glu Met Ala Thr Gly
  65          70          75          80
50 Trp Lys Lys Ile Ala Asp Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala
  85          90          95
Met Lys Thr Gly Trp Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp
  100          105          110
Ala Lys Glu Gly Ala Met Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile
55          115          120          125
Gly Ile Thr Glu Gly Val Met Val Ser Asn Ala Phe Ile Gln Ser Ala
  130          135          140
Asp Gly Thr Gly Trp Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp
145          150          155          160
60 Arg Pro Glu Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu
  165          170          175

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	Leu	Leu	Thr	Val	Leu	Thr	Val	Val	Thr	Gly	Ser	Gly	His	Ala	Ser	Ser
				180					185					190		
	Thr	Pro	Gly	Gly	Glu	Lys	Glu	Thr	Ser	Ala	Thr	Gln	Arg	Ser	Ser	Val
			195					200					205			
5	Pro	Ser	Ser	Thr	Glu	Lys	Asn	Ala	Val	Ser	Met	Thr	Ser	Ser	Val	Leu
		210					215					220				
	Ser	Ser	His	Ser	Pro	Gly	Ser	Gly	Ser	Ser	Thr	Thr	Gln	Gly	Gln	Asp
		225				230					235					240
	Val	Thr	Leu	Ala	Pro	Ala	Thr	Glu	Pro	Ala	Ser	Gly	Ser	Ala	Ala	Thr
10					245					250					255	
	Trp	Gly	Gln	Asp	Val	Thr	Ser	Val	Pro	Val	Thr	Arg	Pro	Ala	Leu	Gly
				260					265					270		
	Ser	Thr	Thr	Pro	Pro	Ala	His	Asp	Val	Thr	Ser	Ala	Pro	Asp	Asn	Lys
			275					280					285			
15	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala
		290					295					300				
	Pro	Asp	Thr	Arg	Pro	Pro	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly
		305				310					315					320
	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Pro	Pro	Gly	Ser	Thr	Ala	Pro
20					325					330					335	
	Ala	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly
				340					345					350		
	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Asn	Arg
			355					360					365			
25	Pro	Ala	Leu	Ala	Ser	Thr	Ala	Pro	Pro	Val	His	Asn	Val	Thr	Ser	Ala
		370					375					380				
	Ser	Gly	Ser	Ala	Ser	Gly	Ser	Ala	Ser	Thr	Leu	Val	His	Asn	Gly	Thr
		385				390					395					400
	Ser	Ala	Arg	Ala	Thr	Thr	Pro	Ala	Ser	Lys	Ser	Thr	Pro	Phe	Ser	
30					405				410					415		
	Ile	Pro	Ser	His	His	Ser	Asp	Thr	Pro	Thr	Thr	Leu	Ala	Ser	His	Ser
				420					425					430		
	Thr	Lys	Thr	Asp	Ala	Ser	Ser	Thr	His	His	Ser	Thr	Val	Pro	Pro	Leu
			435					440					445			
35	Thr	Ser	Ser	Asn	His	Ser	Thr	Ser	Pro	Gln	Leu	Ser	Thr	Gly	Val	Ser
		450					455					460				
	Phe	Phe	Phe	Leu	Ser	Phe	His	Ile	Ser	Asn	Leu	Gln	Phe	Asn	Ser	Ser
		465				470					475					480
40	Leu	Glu	Asp	Pro	Ser	Thr	Asp	Tyr	Tyr	Gln	Glu	Leu	Gln	Arg	Asp	Ile
					485					490					495	
	Ser	Glu	Met	Phe	Leu	Gln	Ile	Tyr	Lys	Gln	Gly	Gly	Phe	Leu	Gly	Leu
				500					505					510		
	Ser	Asn	Ile	Lys	Phe	Arg	Pro	Gly	Ser	Val	Val	Val	Gln	Leu	Thr	Leu
			515					520					525			
45	Ala	Phe	Arg	Glu	Gly	Thr	Ile	Asn	Val	His	Asp	Val	Glu	Thr	Gln	Phe
		530					535					540				
	Asn	Gln	Tyr	Lys	Thr	Glu	Ala	Ala	Ser	Arg	Tyr	Asn	Leu	Thr	Ile	Ser
		545				550					555					560
	Asp	Val	Ser	Val	Ser	Asp	Val	Pro	Phe	Pro	Phe	Ser	Ala	Gln	Ser	Gly
50					565					570					575	
	Ala	Gly	Val	Pro	Gly	Trp	Gly	Ile	Ala	Leu	Leu	Val	Leu	Val	Cys	Val
				580					585					590		
	Leu	Val	Ala	Leu	Ala	Ile	Val	Tyr	Leu	Ile	Ala	Leu	Ala	Val	Cys	Gln
			595					600					605			
55	Cys	Arg	Arg	Lys	Asn	Tyr	Gly	Gln	Leu	Asp	Ile	Phe	Pro	Ala	Arg	Asp
		610					615					620				
	Thr	Tyr	His	Pro	Met	Ser	Glu	Tyr	Pro	Thr	Tyr	His	Thr	His	Gly	Arg
		625				630					635					640
	Tyr	Val	Pro	Pro	Ser	Ser	Thr	Asp	Arg	Ser	Pro	Tyr	Glu	Lys	Val	Ser
60					645					650					655	
	Ala	Gly	Asn	Gly	Gly	Ser	Ser	Leu	Ser	Tyr	Thr	Asn	Pro	Ala	Val	Ala

WO 03/104272

PCT/EP03/06096

Ala Thr Ser Ala Asn Leu
675

665

670

5